```
HUZSIG37    MGSRGQGLLLAYCLLLAFASG----------LVLSRVPHVQGEQQEWEGT ;  40
zacrp5      MAAPALLLLALLLPVGA-------------WPGLPRRP----------- ;  25
ACR3_HUMAN  MLLLGAVLLLLLALP----------------GHDQETTTQGPGVLLPLPK ;  33
HUZSIG39    MRPLLVLLLLGLAAG---------------SPPLDDNKIPSLCP----- ;  29
C1QC_HUMAN  MDVGPSSLPHLGLKLLLLLLLLALRGQA---NTGCY------------- ;  33

HUZSIG37    EELPSPPDHAERAEEQHEKYRPSQDQGLPASRCLRCCDPGTSMYPATAV- ;  89
zacrp5      ------------------------------CVHCCRPAWPPGPYARVS ;  43
ACR3_HUMAN  GACTGWMA----------------------------------------- ;  41
HUZSIG39    ------------------------------------------------- ;  29
C1QC_HUMAN  ------------------------------------------------- ;  33

HUZSIG37    ----------------PQINITILK------------------------ ;  98
zacrp5      DRDLWRGDLWRGLPRVRPTINIEILK---------------------- ;  69
ACR3_HUMAN  ------------------------------------GIPGHPGHN ;  50
HUZSIG39    ----------------------------------GHPGLPGTPGHH ;  41
C1QC_HUMAN  ------------------------GIPGMPGLPGAPGKDGYDGLPGPK ;  57

HUZSIG37    ---------------GEKGDRGDRGLQGKYGKTGSAGARGHTGPKGQKGS ; 133
zacrp5      ---------------GEKGEAGVRGRAGRSGKEGPPGARGLQGRRGQKGQ ; 104
ACR3_HUMAN  GAPGRDGRDGTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGR ; 100
HUZSIG39    GSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGP ;  91
C1QC_HUMAN  GEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPGPMGIPGE ; 107

HUZSIG37    MGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTG ; 183
zacrp5      VGPPGAACRRAYAAFSVGRREGLHSSDHFQAVPFDTELVNLDGAFDLAAG ; 154
ACR3_HUMAN  KGEPGEGAYVYRSAFSVG--LETYVTIPNMPIRFTKIFYNQQNHYDGSTG ; 148
HUZSIG39    TGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTG ; 141
C1QC_HUMAN  PGEEGRYKQKFQSVFTVTR-QTHQPPAPNSLIRFNAVLTNPQGDYDTSTG ; 156

HUZSIG37    KFYCYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVG--DRSIM ; 231
zacrp5      RFLCTVPGVYFLSLNVHTWNYKETYLHIMLNRRPAAVLYAQPS--ERSVM ; 202
ACR3_HUMAN  KFHCNIPGLYYFAYHITVY-MKDVKVSLFKKDKAMLFTYDQYQ--ENNVD ; 195
HUZSIG39    KFTCQVPGVYYFAVHATVY-RASLQFDLVKNGESIASFFQFFGGWPKPAS ; 190
C1QC_HUMAN  KFTCKVPGLYYFVYHASHT--ANLCVLLYRSGVKVVTFCGHTS--KTNQV ; 202

HUZSIG37    QSQ-SLMLELREQDQVWVRLYK-GERENAIFSEELDTYITFSGYLVKHAT ; 279
zacrp5      QAQ-SLMLLLAAGDAVWVRMFQ-RDRDNAIYGEHGDLYITFSGHLVKPAA ; 250
ACR3_HUMAN  QASGSVLLHLEVGDQVWLQVYGEGER-NGLYADN-DNDSTFTGFLLYHDT ; 243
HUZSIG39    LSG-GAMVRLEPEDQVWVQVGV-GDY-IGIYASI-KTDSTFSGFLVYSDW ; 236
C1QC_HUMAN  NSG-GVLLRLQVGEEVWLAVNDYYDM-VGIQGSD----SVFSGFLLFPD- ; 245

HUZSIG37    EP----- ; 281
zacrp5      EL----- ; 252
ACR3_HUMAN  N------ ; 244
HUZSIG39    HSSPVFA ; 243
C1QC_HUMAN  ------- ; 245
```

FIGURE